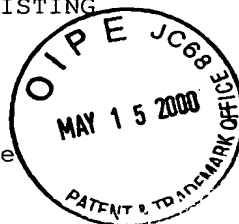


SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANTS: de la Monte, Suzanne  
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
(B) STREET: 1100 New York Ave., Suite 600  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/380,203  
(B) FILING DATE: 25-APR-2000  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/US98/03685  
(B) FILING DATE: 26-FEB-1998
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/038,908  
(B) FILING DATE: 26-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0609.4370001
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1442 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT	TGAG	ATG	GAG	TTT	TCG	CTC	TTG	TTG	CCC	AGG	CTG	GAG	TGC	50		
	Met	Glu	Phe	Ser	Leu	Leu	Leu	Pro	Arg	Leu	Glu	Cys				
	1				5					10						
AAT	GGC	GCA	ATC	TCA	GCT	CAC	GGG	AAC	CTC	CGC	CTC	CCG	GGT	TCA	AGC	98
Asn	Gly	Ala	Ile	Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	
	15					20					25					
GAT	TCT	CCT	GCC	TCA	GCC	TCC	CCA	GTA	GCT	GGG	ATT	ACA	GGC	ATG	TGC	146
Asp	Ser	Pro	Ala	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	
	30					35					40					
ACC	CAC	GCT	CGG	CTA	ATT	TTG	TAT	TTT	TTT	TTA	GTA	GAG	ATG	GAG	TTT	194
Thr	His	Ala	Arg	Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	
	45				50					55					60	
CTC	CAT	GTT	GGT	CAG	GCT	GGT	CTC	GAA	CTC	CCG	ACC	TCA	GAT	GAT	CCC	242
Leu	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	
				65					70					75		
TCC	GTC	TCG	GCC	TCC	CAA	AGT	GCT	AGA	TAC	AGG	ACT	GGC	CAC	CAT	GCC	290
Ser	Val	Ser	Ala	Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	
			80					85					90			
CGG	CTC	TGC	CTG	GCT	AAT	TTT	TGT	GGT	AGA	AAC	AGG	GTT	TCA	CTG	ATG	338
Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	
		95					100					105				
TGC	CCA	AGC	TGG	TCT	CCT	GAG	CTC	AAG	CAG	TCC	ACC	TGC	CTC	AGC	CTC	386
Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	
	110					115					120					
CCA	AAG	TGC	TGG	GAT	TAC	AGG	CGT	GCA	GCC	GTG	CCT	GGC	CTT	TTT	ATT	434
Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	
	125				130					135					140	
TTA	TTT	TTT	TTA	AGA	CAC	AGG	TGT	CCC	ACT	CTT	ACC	CAG	GAT	GAA	GTG	482
Leu	Phe	Phe	Leu	Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	
				145					150					155		
CAG	TGG	TGT	GAT	CAC	AGC	TCA	CTG	CAG	CCT	TCA	ACT	CCT	GAG	ATC	AAG	530
Gln	Trp	Cys	Asp	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	
			160					165						170		

1

CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTTA AACAGTTACA 1339  
TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA 1399  
GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA 1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile  
1 5 10 15  
Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala  
20 25 30  
Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg  
35 40 45  
Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly  
50 55 60  
Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala  
65 70 75 80  
Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu  
85 90 95  
Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp  
100 105 110  
Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp  
115 120 125  
Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu  
130 135 140  
Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp  
145 150 155 160  
His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala  
165 170 175  
Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp  
180 185 190  
Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser  
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro  
210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser  
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu  
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly  
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly  
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met  
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly  
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser  
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn  
340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp  
355 360 365

Ser Gln Thr Pro Asp Leu Arg  
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTTT GAGATGGAGT TTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTGTAGTA	180
GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC	240

TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300  
 TGCCTGGCTA ATTTTTGTGG TAGAAACAGG GTTTCCTGA TGTGCCCCAA GCTGGTCTCC 360  
 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCCTCAGCC 420  
 GTGCCTGGCC TTTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480  
 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540  
 TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600  
 TTTATTTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTACCCAG GCTGGAGTGC 660  
 AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720  
 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT 780  
 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840  
 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCTGACT CCACGCCGGC 900  
 CTATTTTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960  
 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020  
 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080  
 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AACTCCTGA CCTCAGGTGA 1140  
 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200  
 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260  
 TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320  
 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380  
 C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60

CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120  
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180  
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240  
CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCCG GCCTCTGCCT 300  
GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360  
CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420  
TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480  
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540  
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTTAT 600  
TTTTATTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660  
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG 720  
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT 780  
AGTAGAGATG GGGTTTCACC ATGTTGCGCA GGTTGATGCT AGATCTCTTG ACCTTGTGAT 840  
CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC 900  
TATTTTTAAT TTTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960  
ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020  
CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT 1080  
TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140  
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGGTGACGC CTCACCCAGC 1200  
CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260  
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACC AGCCAGTCAC 1320  
ATTTTAAAC AGTTACATCT TTATTTTAGT AACTAGAAA GTGATACGAT AACATGGCGG 1380  
AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19



(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear


(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- 
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 26 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14